



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/889,053C  
Source: 1600  
Date Processed by STIC: 4/21/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT  
MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221  
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

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MAY 24 2004

Raw Sequence Listing Error Summary

Technology Center 2600

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/889,053C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1  Wrapped Nucleic  
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2  Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3  Misaligned Amino  
Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters instead.

4  Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5  Variable Length Sequence(s)  contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6  PatentIn 2.0  
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)  . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7  Skipped Sequences  
(OLD RULES) Sequence(s)  missing. If intentional, please insert the following lines for **each** skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8  Skipped Sequences  
(NEW RULES) Sequence(s)  missing. If intentional, please insert the following lines for **each** skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000

9  Use of n's or Xaa's  
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10  Invalid <213>  
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11  Use of <220>  
Sequence(s)  missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12  PatentIn 2.0  
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13  Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

RECEIVED

AMC - Biotechnology Systems Branch - 09/09/2003

JUN 03 2004

TECHNOLOGY CENTER R3700



RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/889,053C

DATE: 04/21/2004  
TIME: 07:53:27

Input Set : A:\7379P2rev.txt  
Output Set: N:\CRF4\04212004\I889053C.raw

4 <110> APPLICANT: Keough, Thomas W.  
6 Youngquist, Robert S  
9 <120> TITLE OF INVENTION: Methods and Kits for Sequencing Polypeptides  
13 <130> FILE REFERENCE: Methods/Kits for Sequencing Polypeptid  
-> 17 <140> CURRENT APPLICATION NUMBER: US/09/889,053C  
19 <141> CURRENT FILING DATE: 2001-07-11  
23 <160> NUMBER OF SEQ ID NOS: 9  
27 <170> SOFTWARE: PatentIn Ver. 2.0

## STORED SEQUENCES

31 <210> SEQ ID NO: 1  
33 <211> LENGTH: 8  
35 <212> TYPE: PRT  
37 <213> ORGANISM: synthetic construct  
41 <400> SEQUENCE: 1  
43 Ala Ser His Leu Gly Leu Ala Arg  
-> 45 1 5 <insert this number. Do not use TAB  
91 <210> SEQ ID NO: 4  
93 <211> LENGTH: 30  
95 <212> TYPE: PRT  
97 <213> ORGANISM: bovine  
101 <400> SEQUENCE: 4  
-> 103 Phe Val Asn Gln His Leu Cya Gly Ser His Leu Val Glu Ala Leu Tyr  
105 1 5 10 15  
-> 109 Leu Val Cya Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Ala  
111 20 25 30

*invalid response - see item 10 on Error summary sheet*

*This error appears throughout*

*Does Not Comply*  
*Corrected Diskette Needed*  
*Sequence*  
*codes between amino*  
*acid numbers.*

*invalid amino acid designator*  
*Use space characters.*

*some errors*

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/889,053C

DATE: 04/21/2004

TIME: 07:53:28

Input Set : A:\7379P2rev.txt

Output Set: N:\CRF4\04212004\I889053C.raw

17 M:270 C: Current Application Number differs, Replaced Current Application Number

15 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1

103 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1

109 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1